

The Claims Defining the Invention are as Follows

1. A method of analysing a nucleic acid sample obtained from a site comprising the step of pretreating the sample to remove or inactivate contaminating nucleic acids originating from the site.
- 5 2. A method according to claim 1 wherein the contaminating nucleic acid is deoxyribonucleic acid (DNA), ribonucleic acid (RNA), locked nucleic acid (LNA) or protein nucleic acid (PNA).
3. A method according to claim 1 or 2 wherein the contaminating nucleic acid is particularly well adapted for amplification via PCR or some other amplification
10 process.
4. A method according to claim 3 wherein the contaminating nucleic acid is an amplicon derived from a PCR or another DNA amplification process.
5. A method according to any one of claims 1 to 4 wherein the contaminating nucleic acid is degradation resistant.
- 15 6. A method according to any one of claims 1 to 5 wherein the contaminating nucleic acid is synthetic.
7. A method according to any one of claims 1 to 6 wherein the pre-treatment comprises treating the sample to preferentially remove or inactivate nucleic acids that are free or substantially free from other cell components.
- 20 8. A method according to claim 7 wherein the pre-treatment is one or more treatments selected from the group comprising: (i) enzymic treatments; (ii) physical treatments; and (iii) chemical treatments.
9. A method according to claim 8 wherein the enzymic treatments comprise contacting the sample with DNAses, RNAses, exonucleases and/or
25 endonucleases.

10. A method according to claim 8 wherein the physical treatments comprise centrifugation, washing, filtration and/or chromatography such a gel filtration chromatography.
11. A method according to claim 8 wherein the chemical treatments comprise the
5 use of sodium hydroxide, sodium hypochlorite, sodium metabisulphite or ammonium metabisulphite, detergents and/or proprietary products designed to remove nucleic acids form surfaces.
12. A method of analysing a nucleic acid sample obtained from a site comprising the pre-treatment step of contacting the sample with a nucleic acid probe that
10 preferentially binds to the contaminating nucleic acids and renders them removable from the sample.
13. A method according to claim 12 wherein the probes is adapted to hybridise to the amplification product of a positive control from a proprietary nucleic acid amplification kit.
- 15 14. A method according to claim 12 or 13 wherein the nucleic acid probe is labelled.
15. A method according to claim 14 wherein the label is biotin/streptavidin.
16. A method according to any one of claims 12 to 15 further comprising the step of removing the contaminating nucleic acid - probe complex from the sample.
- 20 17. A method according to claim 16 wherein the complex is removed using chromatography.
18. A method according to any one of claims 1 to 17 wherein the method of analysing the nucleic acid sample is PCR, mitochondrial DNA sequencing, single nucleotide polymorphism (SNP) analysis and low copy number PCR.
- 25 19. A method according to claim 1 wherein the pre-treatment comprises removing cell bound contaminating nucleic acids from the sample.

20. A method according to claim 19 wherein the cell bound contaminating nucleic acid is particularly well adapted for amplification via PCR or some other amplification process.
21. A method according to claim 19 or 20 wherein the contaminating nucleic acid
5 is of bacterial origin.
22. A method according to claim 21 wherein the contaminating nucleic acid is bacteria engineered to contain at least one multicopy plasmid comprising at least one amplicon.
23. A method according to any one of claims 19-22 wherein the cell bound
10 contaminating nucleic acid is removed by exposing the nucleic acid in the cells and then removing the nucleic acid.
24. A method according to claim 23 wherein the nucleic acid is exposed by lysing the cells.
25. A method according to claim 23 or 24 wherein the nucleic acid is removed
15 using the pre-treatment steps of any one of claims 7 to 17.
26. A method of characterising the nucleic acids in a sample comprising any one of the methods of claims 1 to 26.
27. A method of screening a nucleic acid sample for contaminants that have been purposefully introduced into the sample, the method comprising the step of
20 treating the sample to locate the contaminants.
28. A method according to claim 27 comprising the use of a detectable probe designed to selectively hybridise to the contaminant.
29. A database comprising the results of an analysis generated from a method according to claim 26.
- 25 30. A DNA fingerprint database according to claim 29.

31. A computerised database according to claim 29 or 30.
32. A nucleic acid analysis kit comprising a means to remove a nucleic acid contaminant from a sample to be subjected to analysis.
33. A kit according to claim 32 wherein said means comprises a labelled probe
5 adapted to bind to the contaminant and thus aid in its removal.
34. A kit according to claim 32 wherein said means comprises an enzyme or chemical that can be added to the sample and inactivate or remove the contaminant preferentially or selectively relative to a target nucleic acid.
35. A method of analysing a nucleic acid sample obtained from a crime scene
10 comprising the step of pretreating the sample to remove or inactivate contaminating nucleic acids originating from the crime scene.
36. A method of analysing a crime scene comprising the step of screening the crime scene for contaminating nucleic acids.
37. A method according to claim 36 comprising the step of taking a sample from a
15 point in the crime scene that would not normally contain nucleic acids.
38. A method according to claim 37 wherein said point is an area surrounding an area in which target nucleic acids would normally be located.
39. A method according to claim 38 wherein the point is adjacent a blood stain.
40. A method of analysing a nucleic acid sample obtained from an animal
20 comprising the step of pretreating the sample to remove or inactivate contaminating nucleic acids.
41. A method of analysing a nucleic acid sample obtained from a plant or part thereof such as a seed comprising the step of pretreating the sample to remove or inactivate contaminating nucleic acids.

42. A method of analysing a nucleic acid sample obtained from a human comprising the step of pretreating the sample to remove or inactivate contaminating nucleic acids originating from the crime scene.